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1 GAATTCCCAA AGACAAAatg gattttcaag tgcagatttt cagcttcctg
51 ctaatacagtgcctcagtcataatatccaga ggacaaattg ttctcaccca
101 gtctccagca atcatgtctg catctccagg ggagaagggtc accatgacct
151 gcagtgccag ctcaagtgtg agttacatga actggtacca gcagaagtca
201 ggcacctccc ccaaagatg gatttatgac acatccaaac tggcttctgg
251 agtccttgcct cacttcagggt gcagtgggtc tgggacctct tactctctca
301 caatcagcgg catggagggt gaagatgctg ccacttatta ctgccagcag
351 tggagtagta acccattcac gttcgggtcgc gggacaaagt tggaaataaa
401 ccgggctgat actgcaccaa ctgtatccat cttcccacca tccagtgagc
451 agttaacatc tggaggtgcc tcagtcgtgt gcttcttgaa caacttctac
501 ccaaagaca tcaatgtcaa gtggaagatt gatggcagtg aacgacaaaa
551 tggcgtcctg aacagttgga ctgatcagga cagcaaagac agcacctaca
601 gcatgagcag caccctcacg ttgaccaagg acgagtatga acgacataac
651 agctataacct gtgaggccac tcacaagaca tcaacttcac ccattgtcaa
701 gagcttcaac aggaatgagt gtTAGAGACA AAGGTCCTGA GACGCCACCA
751 CCAGCTCCCA GCTCCATCCT ATCTTCCCTT CTAAGGTCTT GGAGGCTTCC
801 CCACAAGCGC tTACCACTGT TGCGGTGCTC tAAACCTCCT CCCACCTCCT
851 TCTCCTCCTC CTCCCTTTCC TTGGCTTTTA TCATGCTAAT ATTTGCAGAA
901 AATATTCAAT AAAGTGAGTC TTTGCCTTGA AAAAAAAAAA AAA

Fig. 1(a)

1 MDFOVOIFSF LLISASVIIS RGQIVLTQSP AIMSASPGEK VTMTCSASSS
51 VSYMNWYQQK SGTSPKRWIY DTSKLASGVP AHFRGSGSGT SYSLTISGME
101 AEDAATYYCQ QWSSNPFTFG SGTKLEINRA DTAPTVSIFP PSSEQLTSGG
151 ASVVCFLNNF YPKDINVKWK IDGSRQNGV LNSWTDQDSK DSTYSMSSTL
201 TLTKDEYERH NSYTCEATHK TSTSPIVKSF NRNEC*

Fig. 1(b)

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1 GAATTCCCCT CTCCACAGAC ACTGAAAACCT CTGACTCAAC ATGGAAAGGC
51 ACTGGATCTT TCTACTCCTG TTGTCAGTAA CTGCAGGTGT CCACTCCCAG
101 GTCCAGCTGC AGCAGTCTGG GGCTGAACTG GCAAGACCTG GGGCCTCAGT
151 GAAGATGTCC TGCAAGGCTT CTGGCTACAC CTTTACTAGG TACACGATGC
201 ACTGGGTAAA ACAGAGGCCT GGACAGGGTC TGGAAATGGAT TGGATACATT
251 AATCCTAGCC GTGGTTATAC TAATTACAAT CAGAAGTTCA AGGACAAGGC
301 CACATTGACT ACAGACAAAT CCTCCAGCAC AGCCTACATG CAACTGAGCA
351 GCCTGACATC TGAGGACTCT GCAGTCTATT ACTGTGCAAG ATATTATGAT
401 GATCATTACT GCCTTGACTA CTGGGGCCAA GGCACCACTC TCACAGTCTC
451 CTCAGCCAAA ACAACAGCCC CATCGGTCTA TCCACTGGCC CCTGTGTGTG
501 GAGATACAAC TGGCTCCTCG GTGACTCTAG GATGCCTGGT CAAGGGTTAT
551 TTCCCTGAGC CAGTGACCTT GACCTGGAAC TCTGGATCCC TGTCCAGTGG
601 TGTGCACACC TTCCCAGCTG TCCTGCAGTC TGACCTCTAC ACCCTCAGCA
651 GCTCAGTGAC TGTAACCTCG AGCACCTGGC CCAGCCAGTC CATCACCTGC
701 AATGTGGCCC ACCCGGCAAG CAGCACCAAG GTGGACAAGA AAATTGAGCC
751 CAGAGGGCCC ACAATCAAGC CCTGTCCTCC ATGCAAATGC CCAGCACCTA
801 ACCTCTTGGG TGGACCATCC GTCTTCATCT TCCCTCCAAA GATCAAGGAT
851 GTACTCATGA TCTCCCTGAG CCCCATAGTC ACATGTGTGG TGGTGGATGT
901 GAGCGAGGAT GACCCAGATG TCCAGATCAG CTGGTTTGTG AACAACGTGG
951 AAGTACACAC AGCTCAGACA CAAACCCATA GAGAGGATTA CAACAGTACT
1001 CTCCGGGTGG TCAGTGCCCT CCCCATCCAG CACCAGGACT GGATGAGTGG
1051 CAAGGAGTTC AAATGCAAGG TCAACAACAA AGACCTCCCA GCGCCCATCG
1101 AGAGAACCAT CTCAAAACCC AAAGGGTCAG TAAGAGCTCC ACAGGTATAT
1151 GTCTTGCCTC CACCAGAAGA AGAGATGACT AAGAAACAGG TCACTCTGAC
1201 CTGCATGGTC ACAGACTTCA TGCCTGAAGA CATTTACGTG GAGTGGACCA
1251 ACAACGGGAA AACAGAGCTA AACTACAAGA AACTGAACC AGTCCTGGAC
1301 TCTGATGGTT CTTACTTCAT GTACAGCAAG CTGAGAGTGG AAAAGAAGAA
1351 CTGGGTGGAA AGAAATAGCT ACTCCTGTTT AGTGGTCCAC GAGGGTCTGC
1401 ACAATCACCA CACGACTAAG AGCTTCTCCC GGACTCCGGG TAAATGAGCT
1451 CAGCACCCAC AAAACTCTCA GGTCCAAAGA GACACCCACA CTCATCTCCA
1501 TGCTTCCCTT GTATAAATAA AGCACCCAGC AATGCCTGGG ACCATGTAAA
1551 AAAAAAAAAA AAAGGAATTC

Fig. 2(a)

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OKT 3 HEAVY CHAIN PROTEIN SEQUENCE DEDUCED FROM DNA SEQUENCE

1 MERHWIFLLL LSVTAGVHSQ VQLQQSGAEL ARPGASVKMS CKASGYTFTR
 51 YTMHWVKQRP GQGLEWIGYI NPSRGYTNYN QKFKDKATLT TDKSSSTAYM
 101 QLSSLTSEDS AVYYCARYYD DHYCLDYWGQ GTTLTVSSAK TTAPSVYPLA
 151 PFCGDTTGSS VTLGCLVKGY FPEPVTLTWN SGSLSSGVHT FPAVLQSDLY
 201 TLSSSVTVTS STWPSQSITC NVAHPASSTK VDKKIEPRGP TIKPCPPCKC
 251 PARNLLGGPS VFIFPPKIKD VLMISLSPIV TCVVVDVSED DPDVQISWV
 301 NNVEVHTAQT QTHREDYNST LRVVSALPIQ HQDWMMSGKEF KCKVNNKDLP
 351 APIERTISKP KGSVRAPQVY VLPPPEEEMT KKQVTLTCMV TDFMPEDIYV
 401 EWTNNGKTEL NYKNTEPVLD SDGSYFMYSK LRVEKKNWVE RNSYSCSVVH
 451 EGLHNHHTTK SFSRTPGK*

Fig. 2(b)

	1		23		42
	NN	N	N	N	N
RES TYPE	SBspSPESssBSbSsSSsPSPSPsPSsse*s*p*Pi`ISsSe				
Okt3v1	QIVLTQSPAISASPGKEVMTMTCSASS.SVSYMNWYQQKSGT				
REI	DIQMTQSPSSLSASVGDRTITCQASQDIKYLNWYQQTPGK				
	? ?				
	CDR1	(LOOP)	*****		
	CDR1	(KABAT)	*****		

		56		85
	N	NN		
RES TYPE	*IsiPpIeesesssSBesePsPSBSSEsPspSPsseeSSPePb			
Okt3v1	SPKRWIYDTSKLAGVPAHFRGSGSGTSYSLTISGMEADAAT			
REI	APKLLIYEASNLAQGVPSRFSGSGSGTDYTFITISLQPEDIAI			
	? ?? ? ?			
	***** CDR2 (LOOP/KABAT)			

		102	108
RES TYPE	PiPIPIes**iPIIsPPSPSPSS		
Okt3v1	YYCQQWSSNPFTFGGGTKLEINR		
REIv1	YYCQQYQSLPYTFGQGTKLQITR		
	? ?		
	*****	CDR3 (LOOP)	
	*****	CRD3 (KABAT)	

Fig. 3

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NN N 23 26 32 35 N39 43
 RES TYPE SESPs`SBsss`SSSSpSpSPSPSEbSBssBePiPiesss
 Okt3h QVQLQOSGAELARPGASVKMSCKASGYTFTRYTMHWVKQRPGQ
 KOL QVQLVESGGGVVQPGRSLRLSCSSSGFIFSSYAMYWVRQAPGK
 ? ??
 ***** CDR1 (LOOP)
 ***** CDR1 (KABAT)

52a 60 65 N N N 82abc 89
 RES TYPE IIeIppp`ssssssss`ps`pSSsbSpseSsSseSp`pSpSBSsS`ePb
 Okt3vh GLEWIGYINPSRGYTNTNQKFKDKATLTTDKSSSTAYMQLSSLTSEDSAV
 KOL GLEWVAIIWDDGSDQHYADSVKGRFTISRDNSKNTLFLQMDSLRPEDTGV
 ?? ? ? ? ?
 ***** CDR2 (LOOP)
 ***** CDR2 (KABAT)

92 N 107 113
 RES TYPE PiPiEissssiisssbibib*EIPIP*spSBSS
 Okt3vh YYCARYYDDHY.....CLDYWGQGTTTLTVSS
 KOL YFCARDGGHGFCSSASCFGPDYWGQGTPVTVSS
 ***** CRD3 (KABAT/LOOP)

Fig. 4

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OKT 3 HEAVY CHAIN CDR GRAFTS

1. gh341 and derivatives

	1	26	35	39	43	
Okt3vh	QVQLQQSGAELARPGASVKMSCKASGYTFTRYTMHWVKQRPQG					
gh341	QVQLVESGGGVVQPGRSLRLSCSSSGYTFTRYTMHWVRQAPGK					JA178
gh341A	QVQLVQSGGGVVQPGRSLRLSC <u>KASGYTFTRYTMHWVRQAPGK</u>					JA185
gh341E	QVQLVQSGGGVVQPGRSLRLSC <u>KASGYTFTRYTMHWVRQAPGK</u>					JA198
gh341*	QVQLVQSGGGVVQPGRSLRLSC <u>KASGYTFTRYTMHWVRQAPGK</u>					JA207
gh341*	QVQLVQSGGGVVQPGRSLRLSC <u>KASGYTFTRYTMHWVRQAPGK</u>					JA209
gh341D	QVQLVQSGGGVVQPGRSLRLSC <u>KASGYTFTRYTMHWVRQAPGK</u>					JA197
gh341*	QVQLVQSGGGVVQPGRSLRLSC <u>KASGYTFTRYTMHWVRQAPGK</u>					JA199
gh341C	QVQLVQSGGGVVQPGRSLRLSC <u>KASGYTFTRYTMHWVRQAPGK</u>					JA184
gh341*	QVQLVQSGGGVVQPGRSLRLSCS <u>ASGYTFTRYTMHWVRQAPGK</u>					JA203
gh341*	QVQLVESGGGVVQPGRSLRLSCS <u>ASGYTFTRYTMHWVRQAPGK</u>					JA205
gh341B	QVQLVESGGGVVQPGRSLRLSCSSSGYTFTRYTMHWVRQAPGK					JA183
gh341*	QVQLVQSGGGVVQPGRSLRLSCS <u>ASGYTFTRYTMHWVRQAPGK</u>					JA204
gh341*	QVQLVESGGGVVQPGRSLRLSCS <u>ASGYTFTRYTMHWVRQAPGK</u>					JA206
gh341*	QVQLVQSGGGVVQPGRSLRLSCS <u>ASGYTFTRYTMHWVRQAPGK</u>					JA208
KOL	QVQLVESGGGVVQPGRSLRLSCSSSGFIFSSYAMYWVRQAPGK					

Fig. 5(i)

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	44	50	65	83	
Okt3vh	GLEW	IGYINPSRGY	TNYNQKFKDKATLT	TDKSSSTAYMQLSSLT	
gH341	GLEW	VAYINPSRGY	TNYNOKFKDRFTIS	RDNSKNTLFLQMDSL	JA178
gH341A	GLEW	IGYINPSRGY	TNYNOKVKDRFTIS	TDKSKSTAFLQMDSL	JA185
gH341E	GLEW	IGYINPSRGY	TNYNOKVKDRFTIS	TDKSKSTAFLQMDSL	JA198
gH341*	GLEW	IGYINPSRGY	TNYNOKVKDRFTIS	TDKSKNTAFLQMDSL	JA207
gH341*	GLEW	IGYINPSRGY	TNYNOKVKDRFTIS	RDNSKNTAFLQMDSL	JA209
gH341D	GLEW	IGYINPSRGY	TNYNOKVKDRFTIS	TDKSKNTLFLQMDSL	JA197
gH341*	GLEW	IGYINPSRGY	TNYNOKVKDRFTIS	RDNSKNTLFLQMDSL	JA199
gH341C	GLEW	VAYINPSRGY	TNYNOKFKDRFTIS	RDNSKNTLFLQMDSL	JA184
gH341*	GLEW	IGYINPSRGY	TNYNOKVKDRFTIS	TDKSKSTAFLQMDSL	JA207
gH341*	GLEW	IGYINPSRGY	TNYNOKVKDRFTIS	TDKSKSTAFLQMDSL	JA205
gH341B	GLEW	IGYINPSRGY	TNYNOKVKDRFTIS	TDKSKSTAFLQMDSL	JA183
gH341*	GLEW	IGYINPSRGY	TNYNOKVKDRFTIS	TDKSKSTAFLQMDSL	JA204
gH341*	GLEW	IGYINPSRGY	TNYNOKVKDRFTIS	TDKSKSTAFLQMDSL	JA206
gH341*	GLEW	IGYINPSRGY	TNYNOKVKDRFTIS	TDKSKNTAFLQMDSL	JA208
KOL	GLEW	VAIIWDDGSDQHYADSVKGRFTIS	RDNSKNTLFLQMDSL		

Fig. 5(ii)

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	84	95	102	113	
Okt3vh	SEDS	AVYYCARYYDDHY.....	CLDYWGQGTTLTVSS		
gH341	PEDTGVYFCARYYDDHY.....	CLDYWGQGTTLTVSS			JA178
gH341A	PEDTAVYYCARYYDDHY.....	CLDYWGQGTTLTVSS			JA185
gH341E	PEDTGVYFCARYYDDHY.....	CLDYWGQGTTLTVSS			JA198
gH341*	PEDTGVYFCARYYDDHY.....	CLDYWGQGTTLTVSS			JA207
gH341D	PEDTGVYFCARYYDDHY.....	CLDYWGQGTTLTVSS			JA197
gH341*	PEDTGVYFCARYYDDHY.....	CLDYWGQGTTLTVSS			JA209
gH341*	PEDTGVYFCARYYDDHY.....	CLDYWGQGTTLTVSS			JA199
gH341C	PEDTGVYFCARYYDDHY.....	CLDYWGQGTTLTVSS			JA184
gH341*	PEDTAVYYCARYYDDHY.....	CLDYWGQGTTLTVSS			JA203
gH341*	PEDTAVYYCARYYDDHY.....	CLDYWGQGTTLTVSS			JA205
gH341B	PEDTAVYYCARYYDDHY.....	CLDYWGQGTTLTVSS			JA183
gH341*	PEDTGVYFCARYYDDHY.....	CLDYWGQGTTLTVSS			JA204
gH341*	PEDTGVYFCARYYDDHY.....	CLDYWGQGTTLTVSS			JA206
gH341*	PEDTGVYFCARYYDDHY.....	CLDYWGQGTTLTVSS			JA208
KOL	PEDTGVYFCARDGGHGFCS	SASCFGPDYWGQGTPVTVSS			

Fig. 5(iii)

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OKT3 LIGHT CHAIN CDR GRAFTING

1. gL221 and derivatives

	1	24	34	42
Okt3v1	QIVLTQSPAIMSASPGEKVTMTCSASS.SVSYMNWYQQKSGT			
gL221	DIQMTQSPSSLSASVGDRVTTITCSASS. <u>SVSYMNWYQQTPGK</u>			
gL221A	<u>QIV</u> MTQSPSSLSASVGDRVTTITCSASS.SVSYMNWYQQTPGK			
gL221B	<u>QIV</u> MTQSPSSLSASVGDRVTTITCSASS.SVSYMNWYQQTPGK			
gL221C	DIQMTQSPSSLSASVGDRVTTITCSASS.SVSYMNWYQQTPGK			
REI	DIQMTQSPSSLSASVGDRVTTITCQASQDIKYLWYQQTPGK			
	43	50	56	85
Okt3v1	SPKRWIYDTSKLASGVPAHFRGSGSGTSYSLTISGMEAEDAAT			
gL221	APKLLIYDTSKLASGVPSRFSGSGSGTDYFTFTISSLQPEDIA			
gL221A	APKRWIYDTSKLASGVPSRFSGSGSGTDYFTFTISSLQPEDIA			
gL221B	APKRWIYDTSKLASGVPSRFSGSGSGTDYFTFTISSLQPEDIA			
gL221C	APKRWIYDTSKLASGVPSRFSGSGSGTDYFTFTISSLQPEDIA			
REI	APKLLIYEASNLOAGVPSRFSGSGSGTDYFTFTISSLQPEDIA			
	86	91	96	108
Okt3v1	YYCQWSSNPFTFGSGTKLEINR			
gL221	YYCQWSSNPFTFGQGTKLQITR			
gL221A	YYCQWSSNPFTFGQGTKLQITR			
gL221B	YYCQWSSNPFTFGQGTKLQITR			
gL221C	YYCQWSSNPFTFGQGTKLQITR			
REI	YYCQQYQSLPYTFGQGTKLQITR			

CDR'S ARE UNDERLINED

FRAMEWORK RESIDUES INCLUDED IN THE GENE ARE DOUBLE UNDERLINED

Fig. 6

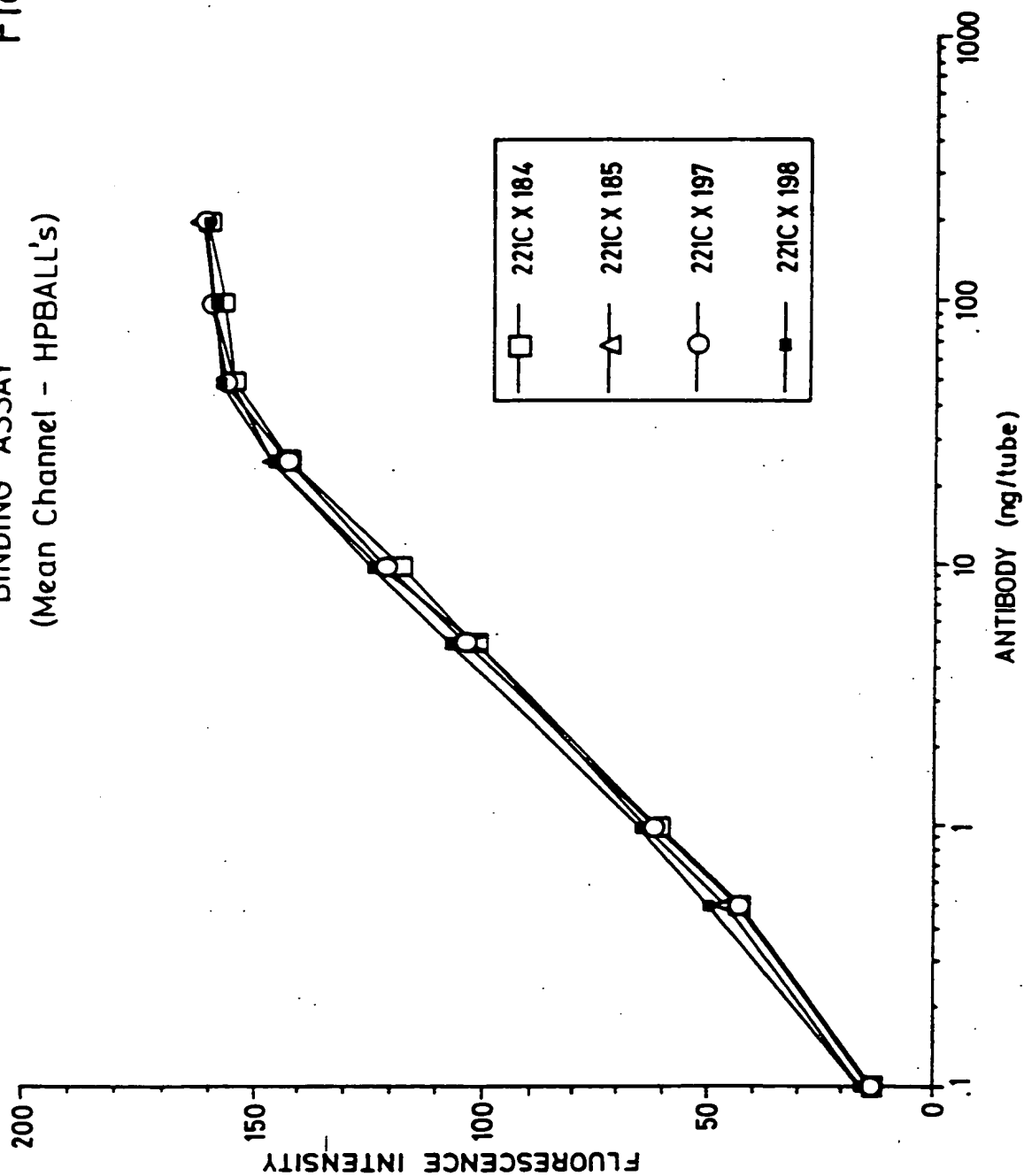
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Fig. 7

OKT3 - pJA198 EVALUATION
BINDING ASSAY
(Mean Channel - HPBALL's)

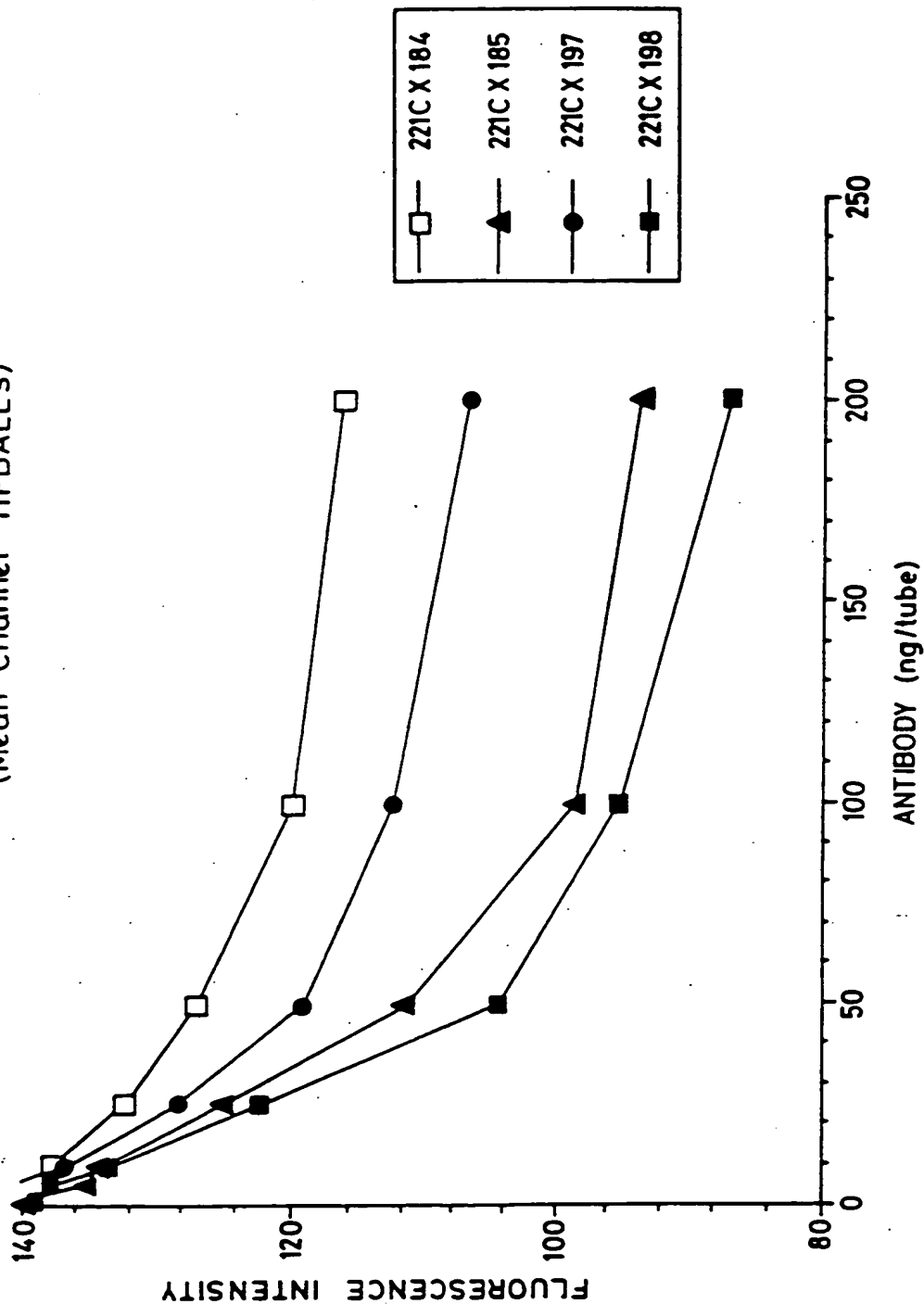


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Fig. 8

OKT3 - pJA198 EVALUATION
BLOCKING ASSAY
(Mean Channel -HPBALL's)



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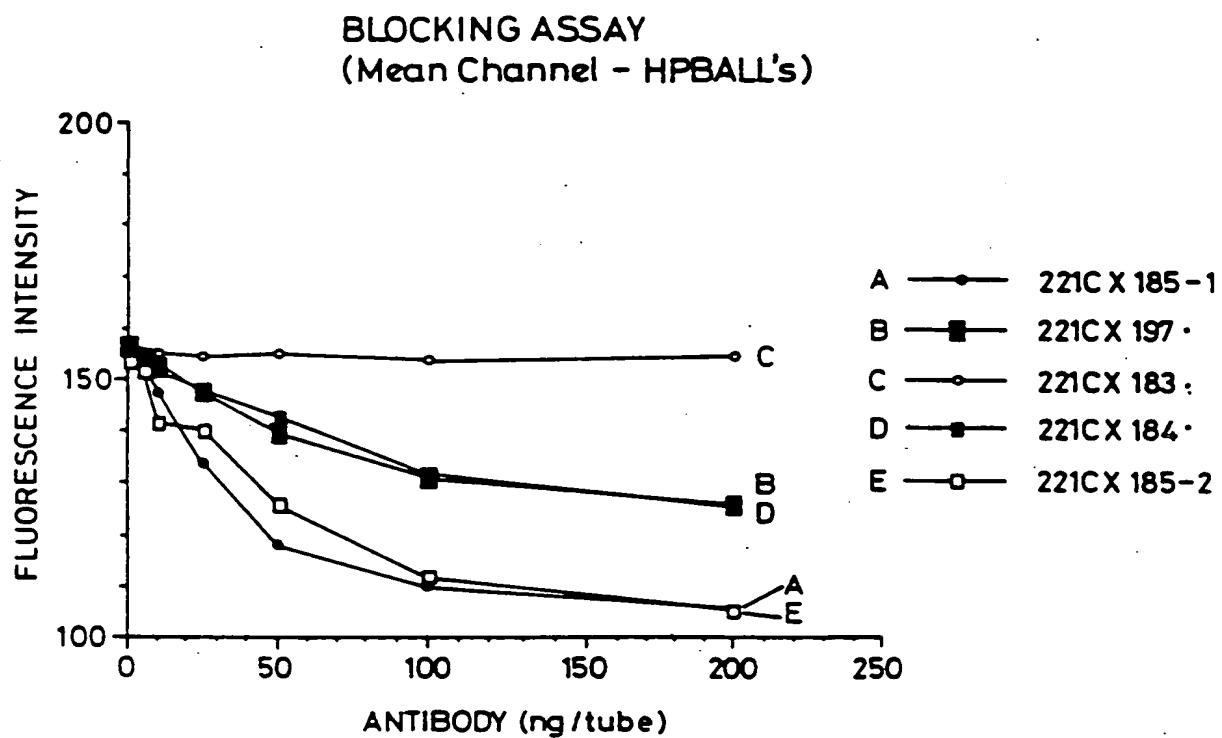
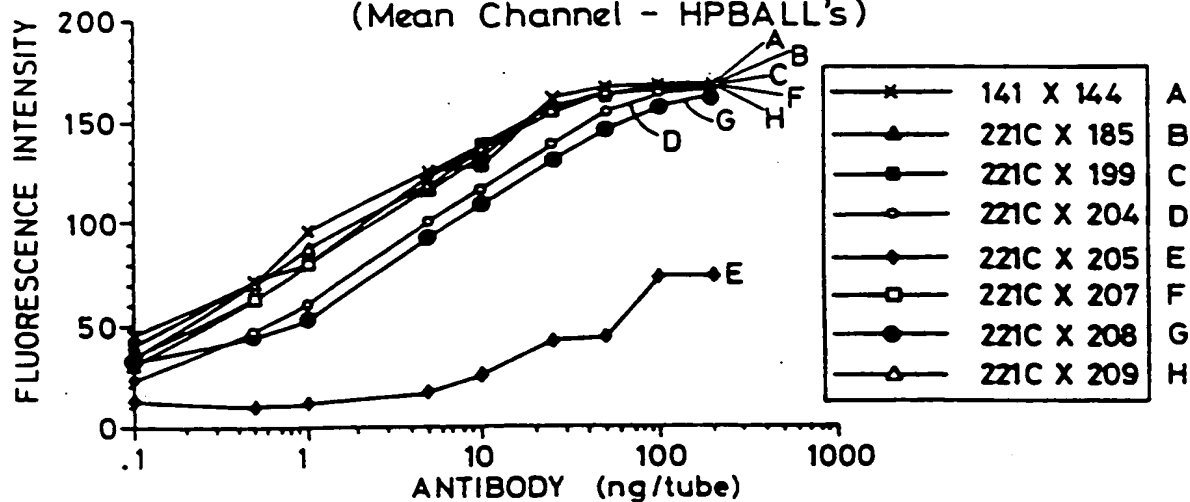


Fig. 9

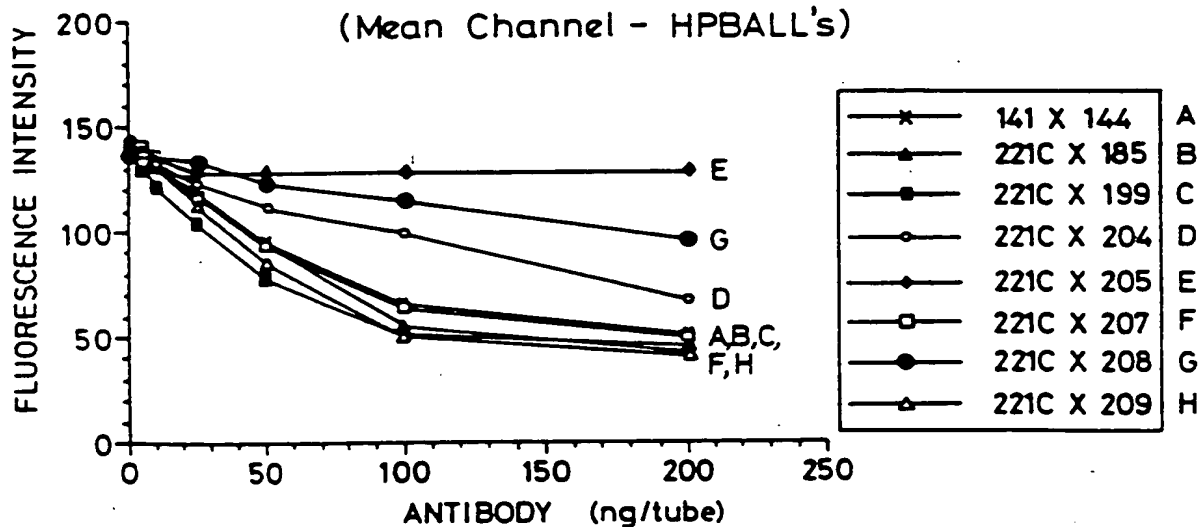
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Fig.10

OKT3 - GRAFTED HEAVY CHAINS
BINDING ASSAY
(Mean Channel - HPBALL's)



OKT3 - GRAFTED HEAVY CHAINS
BLOCKING ASSAY
(Mean Channel - HPBALL's)

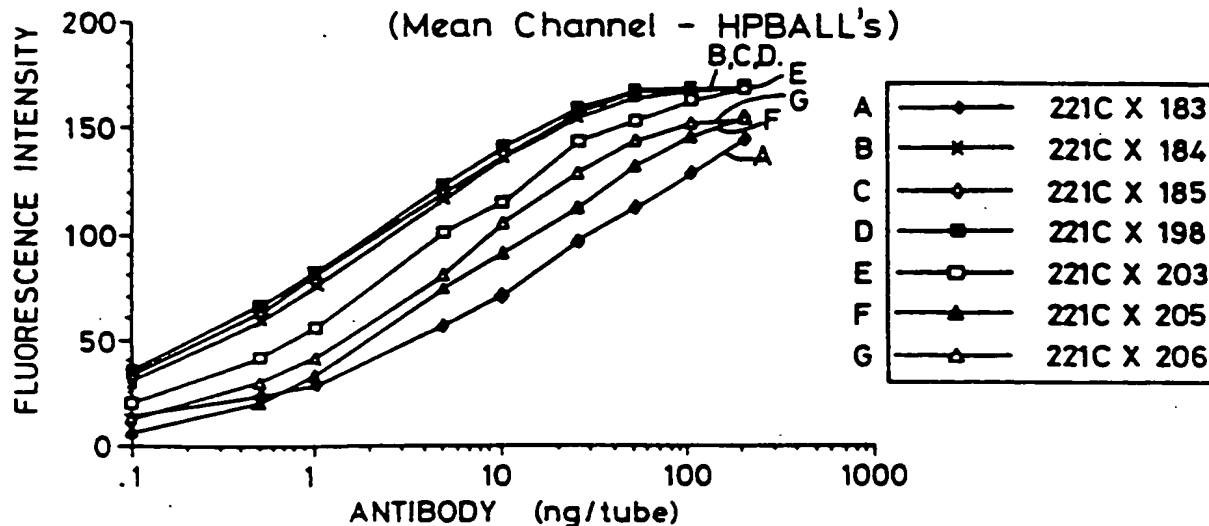


◆	(205)	---,24,48,49,71,73,76,78,88,91,
●	(208)	6,---,24,48,49,71,73,---,78,---,---
○	(204)	6,---,24,48,49,71,73,76,78,---,---
■	(199)	6,23,24,48,49,---,---,---,---,---
□	(207)	6,23,24,48,49,71,73,---,78,---,---
▲	(185)	6,23,24,48,49,71,73,76,78,88,91,
△	(209)	6,23,24,48,49,---,---,---,78,---,---
×	141 X 144	

Fig. 11

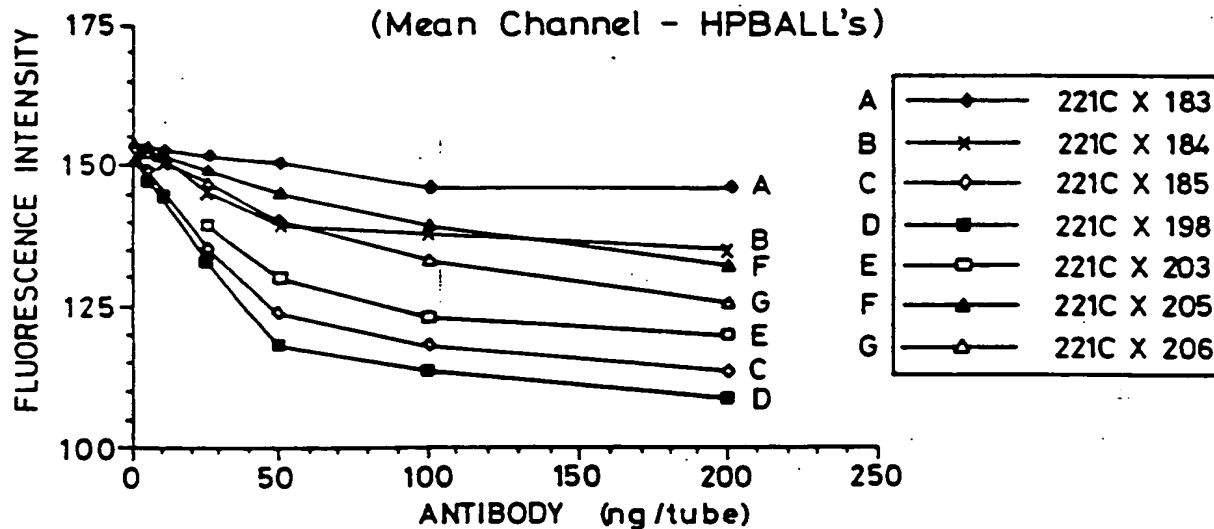
OKT3 - GRAFTED HEAVY CHAINS BINDING ASSAY

(Mean Channel - HPBALL's)



OKT3 GRAFTED HEAVY CHAINS BLOCKING ASSAY

(Mean Channel - HPBALL's)










	(183)	---,---,48,49,71,73,76,78,88,91,
	(205)	---,---,24,48,49,71,73,76,78,88,91,
	(184)	6,23,24,---,---,---,---,---,---,---,
	(206)	---,---,24,48,49,71,73,76,78,---,---,
	(203)	6,---,24,48,49,71,73,76,78,88,91,
	(185)	6,23,24,48,49,71,73,76,78,88,91,
	(198)	6,23,24,48,49,71,73,76,78,---,---,

Fig. 12

OKT3 Competition
Murine Ref Std vs. CDR Grafted OKT3

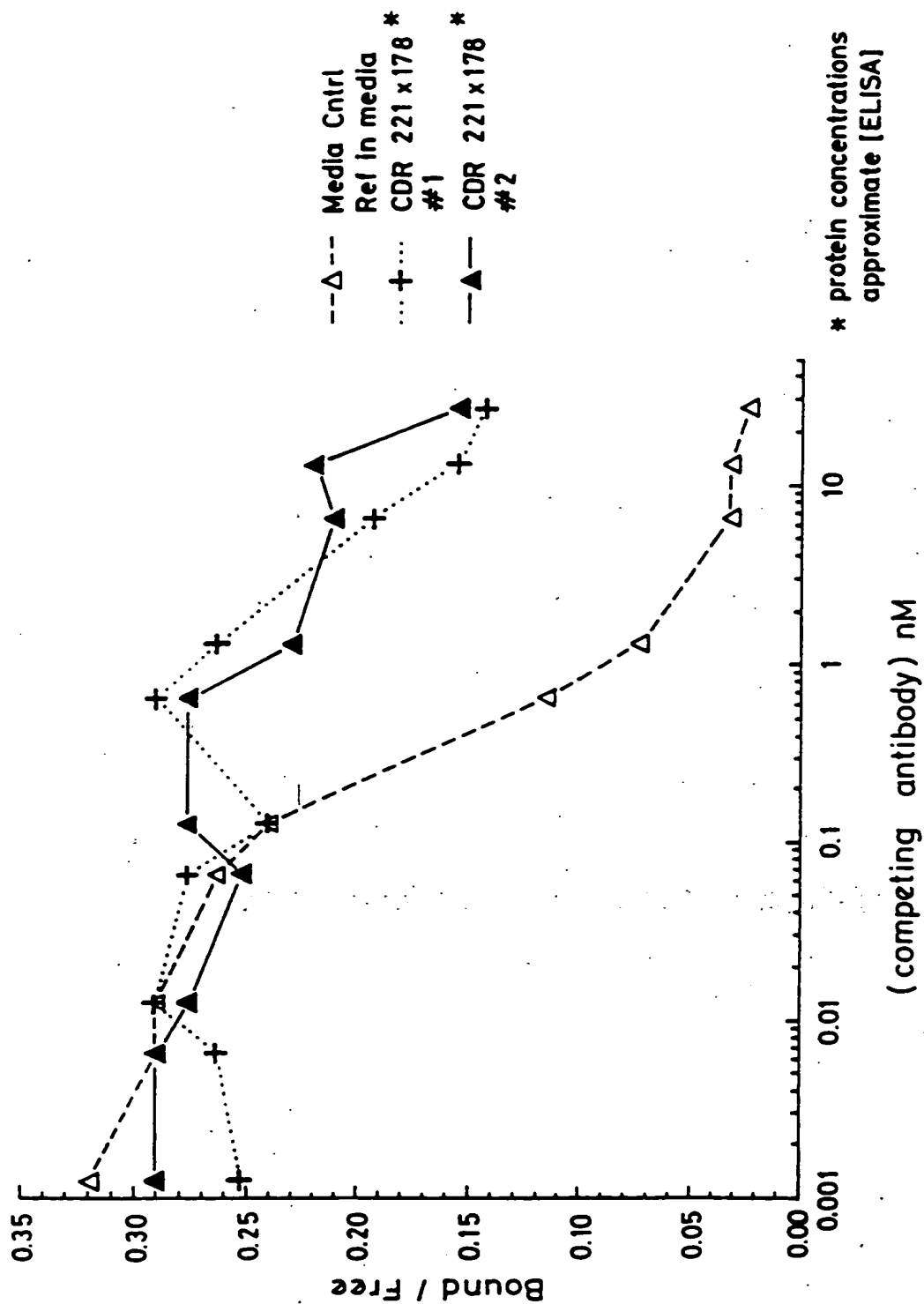


Fig. 13

OKT3 Competition
Murine Ref Std vs. CDR Grafted OKT3

